

TCT	CAC	CGG	GAC	TCG	GGA	CTC	CCG	GGA	AGT	GGA	CCG	GCA	GAA	GAG	GGG	GCT	ACC	54
	9				18			27			36			45				
TAG	CTG	TCT	CTG	CGG	ACC	AGG	GAG	ACC	CCC	GCG	CCC	CGG	TGT	GAG	GCG	GCC		
	63				72			81			90			99			108	
TCA	CAG	GGC	CGG	GTC	GGC	TGG	CGA	GCC	GAC	GCG	GCG	GAG	GAG	GCT	GTG	AGG		
	117				126			135			144			153		162		
AGT	GTG	TGG	AAC	AGG	ACC	CGG	GAC	AGA	GGA	ACC	ATG	GCT	CCG	CAG	AAC	CTG	AGC	
	171				180			189			198		207			216		
ACC	TTT	TGC	CTG	TTG	CTG	CTA	TAC	CTC	ATC	GGG	GCG	GTG	ATT	GCC	GGA	CGA	GAT	
	225				234			243			252			261		270		
T	F	C	L	L	L	L	Y	L	I	G	A	V	I	A	G	R	D	
	279				288			297			306			315		324		
TTC	TAT	AAG	ATC	TTG	GGG	GTG	CCT	CGA	AGT	GCC	TCT	ATA	AAG	GAT	ATT	AAA	AAG	
F	Y	K	I	L	G	V	P	R	S	A	S	I	K	D	I	K	K	
GCC	TAT	AGG	AAA	CTA	GCC	CTG	CAG	CTT	CAT	CCC	GAC	CGG	AAC	CCT	GAT	GAT	CCA	
	333				342			351			360			369		378		
A	Y	R	K	L	A	L	Q	L	H	P	D	R	N	P	D	D	P	

FIGURE 1A

APPROVED	BY	CLASS	SUBCLASS
0.2. FIG.			

CAA GCC CAG GAG AAA TTC CAG GAT CTG GGT GCT GCT TAT GAG GTT CTG TCA GAT	387	396	405	414	423	432
Q A Q E K F Q D L G A A Y E V L S D						
AGT GAG AAA CGG AAA CAG TAC GAT ACT TAT GCT GAA GAA GGA TTA AAA GAT GGT	441	450	459	468	477	486
S E K R K Q Y D T Y G E E G L K D G						
CAT CAG AGC TCC CAT GGA GAC ATT TTT TCA CAC TTC TTT GGG GAT TTT GGT TTC	495	504	513	522	531	540
H Q S S H G D I F S H F F G D F G F						
ATG TTT GGA GGA ACC CCT CGT CAG CAA GAC AGA AAT ATT CCA AGA GGA AGT GAT	549	558	567	576	585	594
M F G G T P R Q Q D R N I P R G S D						
ATT ATT GTA GAT CTA GAA GTC ACT TTG GAA GAA GTA TAT GCA GGA AAT TTT GTG	603	612	621	630	639	648
I I V D L E V T L E E V Y A G N F V						
GAA GTA GTT AGA AAC AAA CCT GTG GCA AGG CAG GCT CCT GGC AAA CGG AAG TGC	657	666	675	684	693	702
E V V R N K P V A R Q A P G K R K C						
AAT TGT CGG CAA GAG ATG CGG ACC ACC CAG CTG GGC CCT GGG CGC TTC CAA ATG	711	720	729	738	747	756
N C R Q E M R T T Q L G P G R R F Q M						

FIGURE 1B

FIGURE 1B shows the sequence of the DNA fragment. The sequence is as follows: CAA GCC CAG GAG AAA TTC CAG GAT CTG GGT GCT GCT TAT GAG GTT CTG TCA GAT. The sequence is shown in the following table:

APPROVED	BY	DRAFTSMAN
C.G. FIG.		CLASS
		SUBCLASS

ACC CAG GAG GTG GTC TGC GAC GAA TGC CCT AAT GTC AAA CTA GTG AAT GAA GAA	765	774	783	792	801	810
T Q E V V C D E C P N V K L V N E E						
CGA ACG CTG GAA GTA GAA ATA GAG CCT GGG GTG AGA GAC GGC ATG GAG TAC CCC	819	828	837	846	855	864
R T L E V E I E P G V R D G M E Y P						
TTT ATT GGA GAA GGT GAG CCT CAC GTG GAT GGG GAG CCT GGA GAT TTA CGG TTC	873	882	891	900	909	918
F I G E G E P H V D G E P G D L R F						
CGA ATC AAA GTT GTC AAG CAC CCA ATA TTT GAA AGG AGA GGA GAT GAT TTG TAC	927	936	945	954	963	972
R I K V V K H P I F E R R G D D L Y						
ACA AAT GTG ACA GTC TCA TTA GTT GAG TCA CTG GTT GGC TTT GAG ATG GAT ATT	981	990	999	1008	1017	1026
T N V T V S L V E S L V G F E M D I						
ACT CAC TTG GAT GGT CAC AAG GTA CAT ATT TCC CGG GAT AAG ATC ACC AGG CCA	1035	1044	1053	1062	1071	1080
T H L D G H K V H I S R D K I T R P						
GGA GCG AAN TAN TGG AAG AAA GGG GAA GGG CTC CCC AAC TTT GAC AAC AAC AAT	1089	1098	1107	1116	1125	1134
G A X X X W K K G E G L P N F D N N N						

FIGURE 1C

100% pure DNA, 100% pure RNA, 100% pure protein, 100% pure lipid, 100% pure carbohydrate, 100% pure mineral, 100% pure vitamin, 100% pure hormone, 100% pure enzyme, 100% pure antibody, 100% pure antigen, 100% pure cell, 100% pure tissue, 100% pure organ, 100% pure system, 100% pure organism, 100% pure population, 100% pure community, 100% pure ecosystem, 100% pure biosphere, 100% pure universe.

APPROVED	BY	DRAFTSMAN
O.G. FIG.		CLASS
		SUBCLASS

1143 1152 1161 1170 1179 1188
 ATC AAG GGC TCT TTG ATA ATC ACT TTT GAT GTG GAT TTT CCA AAA GAA CAG TTA
 I K G S L I I T F D V D F P K E Q L

1197 1206 1215 1224 1233 1242
 ACA GAG GAA GCG AGA GAA GGT ATC AAA CAG CTA CTG AAA CAA GGG TCA GTG CAG
 T E E A R E G I K Q L L K Q G S V Q

1251 1260 1269 1278 1287 1296
 AAG GTA TAC AAT GGA CTG CAA GGA TAT TGA GAG TGA ATA AAA TTG GAC TTT GTT
 K V Y N G L Q G Y

1305 1314 1323 1332 1341 1350
 TAA AAT AAG TGA ATA AGC GAT ATT TAT TAT CTG CAA GGT TTT TTT GTG TGT GTT

1359 1368
 TTT GTT TTT ATT TTC AAT ATG CAA GT

FIGURE 1D

1143 1152 1161 1170 1179 1188
 ATC AAG GGC TCT TTG ATA ATC ACT TTT GAT GTG GAT TTT CCA AAA GAA CAG TTA
 I K G S L I I T F D V D F P K E Q L

[illegible]

FIGURE 2A

APPROVED	BY	DRAFTSMAN
0.6 FIG.	CLASS	SUBCLASS

254 R G D D L Y T N V T V S L V E S L V G F F E M D I T T H L D G H K V H I S R D - - K 136466

254 R G E D L F M C M D I Q L V E A L C G F Q K P I S T L D N R T I V I T S H P G Q G I 306714

292	I	T	R	P	G	A	X	X	W	K	G	E	G	L	P	N	F	D	N	N	I	K	G	S	L	I	I	T	F	D	V	D	F	P	K	E	O	L	136466		
294	I	V	K	H	G	D	I	K	C	V	L	N	E	G	M	P	I	Y	R	R	P	Y	E	K	G	R	L	I	I	E	F	K	V	N	F	P	E	N	G	F	GI 306714

332	<u>T E A R E G I</u>	- - - - -	<u>K O L L K Ö G S V Ö K V</u>	- - - - -	136466
334	L S P D K L S L E K L L P E R		K E V E E T D E M D Q V E L V D F D P N Q E R R G I		306714

352 - - Y N G L O G Y 136466

374 R H Y N G - E A Y E D D E H H P R G G V Q C Q T S GI 306714

FIGURE 2B

[illegible]

CGN	AGG	AGA	GNA	AAG	GAA	AGN	CGC	CGC	AGG	AGC	CGC	CGC	NAC	CAC	CAG	CGN	CAC
		9			18			27			36			45			54

ANT	CCT	GGN	GCT	NTG	AGG	AGA	TTC	GGG	CCG	TCA	CCC	TGC	CTC	CCC	TGC	TTC	CCG
	63			72			81		90		99					108	

	117	126	135	144	153	162
CCA	CCG	GCC	GCT	TCT	TTC	CTC
GGA	CCC	ATT	CCA	ACA	ATC	TCG
TAA	AAC	ATG	GTG			
M	V					

D	Y	Y	E	V	L	G	V	Q	R	H	A	S	P	E	D	I	K
GAT	TAC	TAT	GAA	GTT	CTA	GCC	GTG	CAG	AGA	CAT	GCC	TCA	CCC	GAG	GAT	ATT	AAA
	171				180			189			198			207			216

	225	234	243.	252	261	270
AAG GCA TAT CGG AAA CTG GCA CTG AAG TGG CAT CCA GAT AAA AAT CCT GAG AAT						
K A Y R K L A L K W H P D K N P E N						

AAA	GAA	GAA	GCA	GAG	AGA	AAA	TTC	AAG	CAA	GTA	GGC	GAG	GCA	TAT	GAA	GTG	CTG
K	E	E	A	E	R	K	F	K	Q	V	A	E	A	Y	E	V	L
	279				288			297		306			315			324	

333	342	351	360	369	378
TCG GAT GCT AAG AAA CGG GAC ATC TAT GAC AAA TAT GGC AAA GAA GGA TTA AAT					
S D A K K R D I Y D K Y G K E G L N					

FIGURE 3A

APPROVED	O.G. FIG.	CLASS	SUBCLASS
BY			
DRAFTSMAN			

GGT	GGN	GGN	GGN	GGT	GGA	AGT	CAT	TTT	GAC	AGT	CCA	TTT	GAA	TTT	GGC	TTC	ACA	387	396	405	414	423	432
G	G	G	G	G	G	S	H	F	D	S	P	F	E	F	G	F	T						
TTT	CGT	AAC	CCA	GAT	GAT	GTC	TTC	AGG	GAA	TTT	TTT	GGT	GGA	AGG	GAC	CCA	TTT	441	450	459	468	477	486
F	R	N	P	D	D	V	F	R	E	F	F	G	G	R	D	P	F						
TCA	TTT	GAC	TTC	TTT	GAA	GAC	CCT	TTT	GAG	GAC	TTC	TTT	GGG	AAT	CGA	AGG	GGT	495	504	513	522	531	540
S	F	D	F	F	E	D	P	F	E	D	F	F	G	N	R	R	G						
CCC	CGA	GGA	AGC	AGA	AGC	CGA	GGG	ACG	GGG	TCG	TTT	TTC	TCT	GCG	TTC	AGT	GGA	549	558	567	576	585	594
P	R	G	S	R	S	R	G	T	G	S	F	F	S	A	F	S	G						
TTT	CCG	TCT	TTT	GGA	AGT	GGA	TTT	TCT	TCT	TTT	GAT	ACA	GGA	TTT	ACT	TCA	TTT	603	612	621	630	639	648
F	P	S	F	G	S	G	F	S	S	F	D	T	G	F	T	S	F						
GGG	TCA	CTA	GGT	CAC	GGG	GGC	CTC	ACT	TCA	TTC	TCT	TCC	ACG	TCA	TTT	GGT	GGT	657	666	675	684	693	702
G	S	L	G	H	G	G	L	T	S	F	S	S	T	S	F	G	G						
AGT	GGC	ATG	GGC	AAC	TTC	AAA	TCG	ATA	TCA	ACT	TCA	ACT	AAA	ATG	GTT	AAT	GGC	711	720	729	738	747	756
S	G	M	G	N	F	K	S	I	S	T	S	T	K	M	V	N	G						

FIGURE 3B

APPROVED		BY	DRAFTSMAN
O.G. FIG.		CLASS	SUBCLASS

1143 1152 1161 1170 1179 1188
 CTA GAC CGG ACT TGA GGC ACG CGG TGC ACC CCC AGA CGC TGG CGC TCC ACC GTG
 L D R T

1197 1206 1215 1224 1233 1242
 CTC GGC ATG CGG TCG TGC ACA CGC GCT AGG TAG CAG CGT CGG TCA GGA CTG TCT

1251 1260 1269 1278 1287 1296
 CGA GGC CAC ACT CGC TCG GCA GGA TTA TGC GAT CAC GGA TCA GTC AGA GCA GGG

1305 1314 1323
 TCA GGA GAC GGG GCT GAC GGC ACG GGT GGC GGG G

FIGURE 3D

41	E	A	E	R	K	F	K	O	V	A	E	A	Y	E	V	L	S	D	A	K	K	R	D	I	Y	D	K	Y	G	K	E	G	L	N	G	G	G	G	G	G	260873
41	F	A	E	K	K	F	K	E	V	A	E	A	Y	E	V	L	S	D	K	H	K	R	E	I	Y	D	R	Y	G	R	E	E	G	L	T	G	T	G	T	G	GI 32469
41	F	A	E	K	K	F	K	E	V	A	E	A	Y	E	V	L	S	D	K	H	K	R	E	I	Y	D	R	Y	G	R	E	E	G	L	T	G	T	G	T	G	GI 32470

81	S	H	F	D	S	P	F	E	-	-	F	G	F	T	F	R	N	P	D	D	V	F	R	E	F	F	G	G	R	D	P	F	S	F	D	F	F	E	D	260873
81	S	R	A	E	A	G	S	G	G	P	G	F	T	F	T	R	S	P	E	E	V	F	R	E	F	F	G	S	G	D	P	F	A	-	E	L	F	D	D	GI 32469
81	S	R	A	E	A	G	S	G	G	P	G	F	T	F	T	R	S	P	E	E	V	F	R	E	F	F	G	S	G	D	P	F	A	-	E	L	F	D	D	GI 32470

118	-	P	F	E	D	F	F	G	N	R	R	G	P	R	G	S	R	S	R	G	T	G	S	F	F	S	A	F	S	G	F	P	S	F	G	S	G	F	S	260873
120	L	G	P	F	S	E	L	-	-	Q	N	R	G	-	-	-	-	S	R	H	S	G	P	F	F	T	-	-	-	-	-	F	S	S	S	F	P	GI 32469		
120	L	G	P	F	S	E	L	-	-	Q	N	R	G	-	-	-	-	S	R	H	S	G	P	F	F	T	-	-	-	-	-	F	S	S	S	F	P	GI 32470		

156	S	F	D	T	G	F	T	S	F	G	S	L	G	H	G	G	L	T	S	F	S	S	T	S	F	G	-	G	S	G	M	G	N	F	K	S	I	S	T	S	260873	
146	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	H	S	D	F	S	S	S	S	S	S	S	F	S	P	G	A	G	A	F	R	S	V	S	T	S	GI 32469
146	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	H	S	D	F	S	S	S	S	S	S	S	F	S	P	G	A	G	A	F	R	S	V	S	T	S	GI 32470

195	T	K	M	V	N	G	R	K	I	T	T	K	R	I	V	E	N	G	Q	E	R	V	E	V	E	E	D	G	Q	L	K	S	L	T	I	N	G	V	A	D	260873
171	T	T	F	V	Q	G	R	R	I	T	T	R	R	I	M	E	N	G	Q	E	R	V	E	V	E	E	D	G	Q	L	K	S	V	T	I	N	G	V	P	D	GI 32469
171	T	T	F	V	Q	G	R	R	I	T	T	R	R	I	M	E	N	G	Q	E	R	V	E	V	E	E	D	G	Q	L	K	S	V	T	I	N	G	V	P	D	GI 32470

[illegible]

[illegible][illegible][illegible]

FIGURE 4B